

10/019541

1

SEQUENCE LISTING

<110> Herbers, Karin
Badur, Ralf
Kunze, Irene
Geiger, Michael
Mock, Hans-Peter

<120> Identification and overexpression of a DNA sequence encoding a
2-methyl-6-phytylhydroquinone methyltransferase in
plants.

<130> 0817/00001

<140> US 10/019,541

<150> PCT/EP/00/05862

<151> 2000-06-23

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<170> WordPerfect version 6.1

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<212> DNA

<213> Synechocystis PCC6803

<220>

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Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln Ser	
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tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac ggc att	144
Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile	
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ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat ggc gat	192
Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp	
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ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt gtc cat	240
Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His	
65 70 75 80	
gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc aca acg	288
Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr	
85 90 95	
gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att ctc gcc	336
Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala	

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gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt ttc gac Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp 145 150 155 160			480
gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa gct gtg Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val 165 170 175			528
ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att ctg gtg Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val 180 185 190			576
gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc aac ttc Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe 195 200 205			624
tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc cac cct Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro 210 215 220			672
gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc acg ggt Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly 225 230 235 240			720
ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg acc ctc Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu 245 250 255			768
ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc cag ggc Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly 260 265 270			816
tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg gaa gta Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val 275 280 285			864
ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt tgt cgc Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg 290 295 300			912
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<213> Synechocystis PCC6803

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 35 40 45
 Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
 50 55 60
 Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His
 65 70 75 80
 Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr
 85 90 95
 Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala
 100 105 110
 Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
 115 120 125
 Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
 130 135 140
 Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
 145 150 155 160
 Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
 165 170 175
 Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
 180 185 190
 Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
 195 200 205
 Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
 210 215 220
 Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
 225 230 235 240
 Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
 245 250 255
 Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
 260 265 270
 Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
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 Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg
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tcc ctg gcg atc gcc gct gga ctg tat ctc cta act gcc cgg ggc tat 96
Ser Leu Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr
  15             20             25             30

cag tca tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac 144
Gln Ser Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp
        35             40             45

ggc att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat 192
Gly Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr
        50             55             60

ggc gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt 240
Gly Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe
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gtc cat gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc 288
Val His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly
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Thr Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile
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ctc gcc aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc 384
Leu Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro
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Gln Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala
        130            135            140

aag ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt 480
Lys Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser
        145            150            155

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gct gtg ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att 576

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Ala Val Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile
 175 180 185 190

ctg gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc 624
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 195 200 205

aac ttc tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc 672
 Asn Phe Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser
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cac cct gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc 720
 His Pro Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala
 225 230 235

acg ggt ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg 768
 Thr Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro
 240 245 250

acc ctc ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc 816
 Thr Leu Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro
 255 260 265 270

cag ggc tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg 864
 Gln Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg
 275 280 285

gaa gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt 912
 Glu Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu
 290 295 300

tgt cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct 960
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 35 40 45

Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
 50 55 60

Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His
 65 70 75 80

Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr
 85 90 95
 Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala
 100 105 110
 Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
 115 120 125
 Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
 130 135 140
 Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
 145 150 155 160
 Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
 165 170 175
 Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
 180 185 190
 Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
 195 200 205
 Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
 210 215 220
 Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
 225 230 235 240
 Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
 245 250 255
 Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
 260 265 270
 Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
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 Ser Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly
 15 20 25 30

att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat ggc 147
 Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly
 35 40 45

gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt gtc 195
 Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val
 50 55 60

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 His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr
 65 70 75

acg gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att ctc 291
 Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu
 80 85 90

gcc aaa gat tat ggt ttt aac gtt acc gcc atc acc att agt ccc caa 339
 Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln
 95 100 105 110

cag gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc aag 387
 Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys
 115 120 125

ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt ttc 435
 Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe
 130 135 140
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 Asp Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala
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 160 165 170
 gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc aac 579
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 195 200 205
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 210 215 220
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 Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr
 225 230 235
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 240 245 250
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 Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu
 255 260 265 270
 gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt tgt 867
 Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys
 275 280 285
 cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct taa 915
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 35 40 45
 Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His Ala
 50 55 60
 Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr Val
 65 70 75 80
 Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala Lys
 85 90 95
 Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln Val
 100 105 110
 Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe Ala
 115 120 125
 Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp Val
 130 135 140
 Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val Phe
 145 150 155 160
 Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val Val
 165 170 175
 Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe Trp
 180 185 190
 Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro Ala
 195 200 205
 Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly Leu
 210 215 220
 Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu Pro
 225 230 235 240
 Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly Trp
 245 250 255
 Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val Pro
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